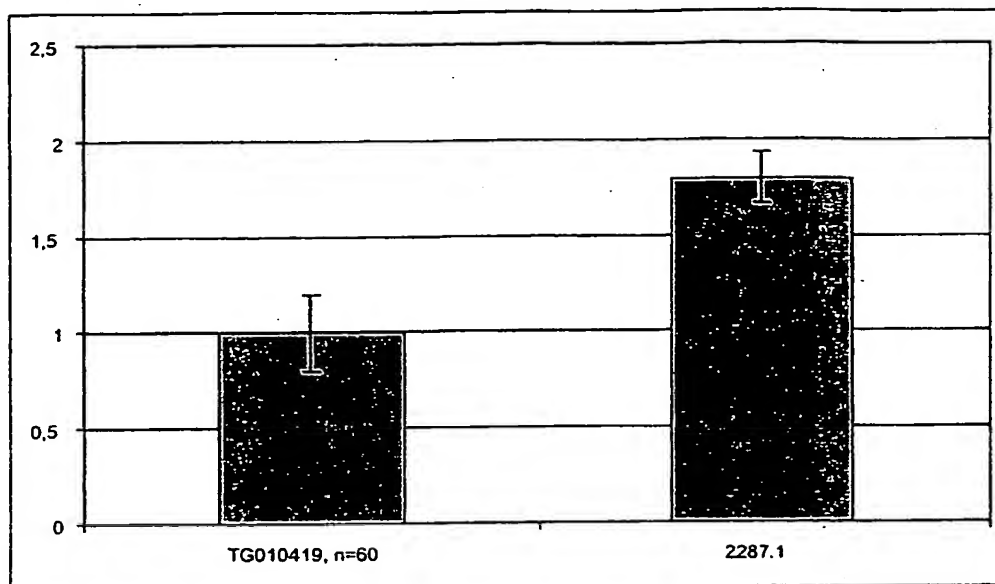


FIGURE 1. Triglyceride content of a CG3842 mutant

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FIGURE 2. Molecular organisation of the gene CG3842 (GadFly Accession Number)

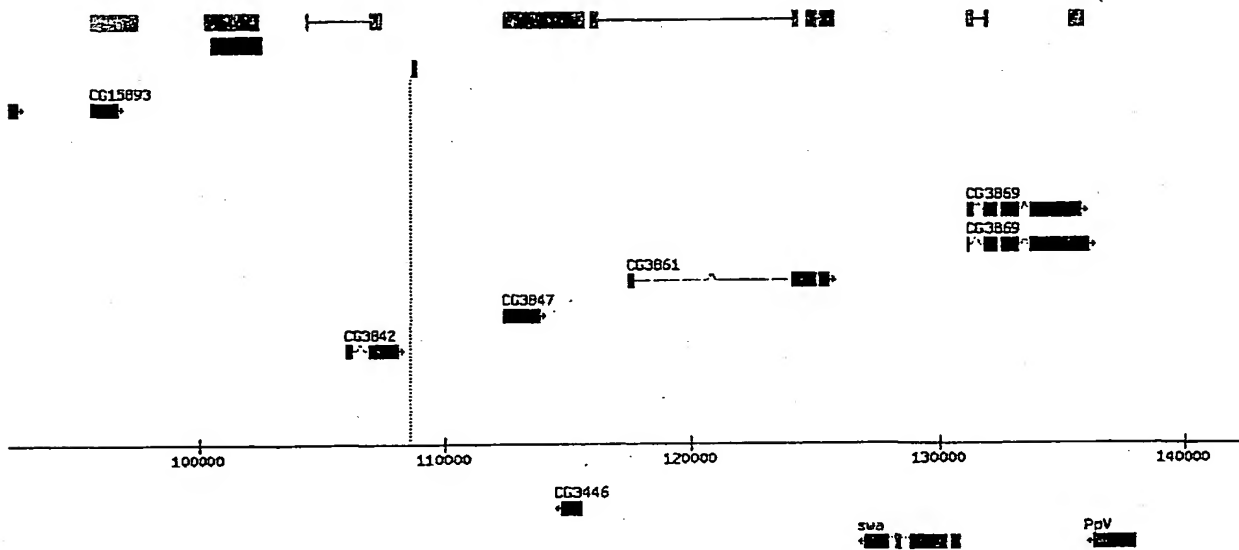


FIGURE 3. BLASTP RESULTS FOR CG3842

FIGURE 3A. Homology to human gene ref XM_085058, protein ref XP_085058.1

>ref|XP_085058.1| (XM_085058) similar to unnamed protein product [Homo sapiens]
 dbj|BAB70811.1| (AK054835) unnamed protein product [Homo sapiens]
 Length = 316

Score = 266 bits (681), Expect = 2e-70
 Identities = 163/317 (51%), Positives = 206/317 (64%), Gaps = 13/317 (4%)

Query: 45 LIVLGILL----FMWL----LRKCIQGPAYRKANRIDGKVVIVTGCNTGIGKETVLELAK 96
 L+ LG+L F+++ +RK G R ++ GKVV++TG NTGIGKET ELA
 Sbjct: 2 LVTLGLLTSFFSFLYMVAPSIRKFFAGGVCRTNVQLPGKVVVITGANTGIGKETARELAS 61

Query: 97 RGARVYMACRDPGRCEAARLDIMDRSRNQQLFNRTLDLGLSLQSVRNFRVERFKAESRLDI 156
 RGARVY+ACRD + E+A +I ++N Q+ R LDL +S+R F E F AEE +L I
 Sbjct: 62 RGARVYIACRDVLKGESAAASEIRVDTKNSQVLVRKLDLSDTKSIRAFAGFLAEEKQLHI 121

Query: 157 LINNAGVMACPRTLTADGFEQQFGVNHGLGHFLLTNLLDLRLKHSSPSRIVVSSAAHLFG 216
 LINNAGVM CP + TADGFE GVNHLGHFLLT LLL+RLK S+P+R+V VSS AH G
 Sbjct: 122 LINNAGVMCPYSKTDGFEHLGVNHGLGHFLLTYLLERLKVSA PARVVNVSSVAHHIG 181

Query: 217 RINREDLMSEKNYSKFFGAYSQSKLANILFTLKLSTILKDTGVTNCCHPGVVRTEINRH 276
 +I DL SEK YS+ F AY SKLAN+LFT +L+ L+ TGVV HPGVVR+E+ RH
 Sbjct: 182 KIPFHDQLSEKRYSRGF-AYCHSKLANVLTRELAKRLQGTGVTTYAVHPGVVRSELVRH 240

Query: 277 FSGPGWMKTALQKGSLYFFKTPKAGAQTLRLALDPQLEGSTGGYYSDCMRWPLFPWVRN 336
 S + L + F KT + GAQT L AL LE +G Y+SDC R + P RN
 Sbjct: 241 SS----LLCLLWRLFSFPVKTA REGAQTSLHCALEGLEPLSGKYFSDCKRTWVSPRARN 296

Query: 337 MQTADWLWRESEKLLGL 353
 +TA+ LW S +LLG+
 Sbjct: 297 NKTAERLWNVSCCELLGI 313

FIGURE 3B. Homology to human gene ref NM_020905, protein ref NP_065956.1

>ref|NP_065956.1| (NM_020905) PAN2 protein [Homo sapiens]
 gb|AAG12190.1|AF237952_1 (AF237952) PAN2 [Homo sapiens]
 gb|AAH09830.1|AAH09830 (BC009830) PAN2 protein [Homo sapiens]
 Length = 336

Score = 254 bits (648), Expect = 1e-66
 Identities = 152/319 (47%), Positives = 191/319 (59%), Gaps = 20/319 (6%)

Query: 54 MWLLRKCIQGPAYRKANR-----IDGKVVIVTGCNTGIGKETVLELAKRGARVYMACRD 107
 +WL + GP ++ R + GK V++TG N+G+G+ T EL + GARV M CRD
 Sbjct: 17 LWLAARRFVGPRVQRLRRGGDPGLMHGKTVLITGANSGLGRATAAELLRLGARVIMGCRD 76

Query: 108 PGRCEAARLDIMDRSRNQ-----QLFNRTLDLGLSLQSVRNFRVERFKAESRL 154
 R E A + R +L R LDL SL+SVR F + EE RL
 Sbjct: 77 RARAEAAAGQLRRELROAAECGPEPGVSGVGELIVRELDLASLRSVRAFCQEMLQEEPRL 136

Query: 155 DILINNAGVMACPRTLTADGFEQQFGVNHGLGHFLLTNLLDLRLKHSSPSRIVVSSAAHL 214
 D+LINNAG+ CP T DGFE QFGVNHGLGHFLLTNLL LK S+PSRIVVSS +
 Sbjct: 137 DVLINNAGIFQCPYMKTEDGFEMQFGVNHGLGHFLLTNLLGLLKSSAPSRIVVSSKLYK 196

Query: 215 FGRINREDLMSEKNYSKFFGAYSQSKLANILFTLKLSTILKDTGVTNCCHPGVVRTEIN 274
 +G IN +DL SE++Y+K F YS+SKLANILFT +L+ L+ T VTN HPG+VRT +
 Sbjct: 197 YGDINFDDLNSEQSYNKS F-CYSRSKLANILFTRELARLEGTVNVTNVLHPGIVRTNLG 255

Query: 275 RHFSGPGWMKTALQKGSLYFFKTPKAGAQTLRLALDPQLEGSTGGYYSDCMRWPLFPWV 334
 RH P +K S FFKTP GAQT + LA P++EG +G Y+ DC L P
 Sbjct: 256 RHIHPLLVKPLFNLVSWAFFKTPVEGAQTSIYLASSPEVEGVSGRYFGDCKEEELLPKA 315

Query: 335 RNMQTADWLWRESEKLLGL 353
 + A LW SE ++GL
 Sbjct: 316 MDESVARKLWDISEVMVGL 334

FIGURE 3C. Homology to human gene ref NM_016026, protein ref NP_057110.1

Pairwise alignment of Drosophila CG3842 encoded protein (query) and androgen-regulated short-chain dehydrogenase/reductase I; prostate short-chain dehydrogenase reductase I; CGI-82 protein [Homo sapiens] (subject)

```
>ref|NP_057110.1| (NM_016026) CGI-82 protein; likely ortholog of mouse cell line
MC/9.IL4 derived transcript 1 [Homo sapiens]
ref|XP_031073.1| (XM_031073) CGI-82 protein [Homo sapiens]
gb|AAD34077.1|AF151840_1 (AF151840) CGI-82 protein [Homo sapiens]
gb|AAH00112.1|AAH00112 (BC000112) CGI-82 protein [Homo sapiens]
gb|AAK72049.1|AF395068_1 (AF395068) HCV core-binding protein HCBP12 [Homo sapiens]
gb|AAH11727.1|AAH11727 (BC011727) Similar to CGI-82 protein [Homo sapiens]
Length = 318
```

Score = 250 bits (638), Expect = 2e-65

Identities = 157/314 (50%), Positives = 196/314 (62%), Gaps = 7/314 (2%)

```
Query: 43  IFLIVLGILLFMWL--LRKCIQGPAYRKANRIDGKVVIVTGCNTGIGKETVLELAKRGAR 100
      + L++L LL+M      +RK +          ++ GKVV+VTG NTGIGKET ELA+RGAR
Sbjct: 8   LLLLLLPFLLYMAAPQIRKMLSSGVCTSTVQLPGKVVVVTGANTGIGKETAKELAQRGAR 67
```

```
Query: 101 VYMACRDPGRCEAARLDIMDRSRNQQLFNRTLGLSLQSVRNFFVERFKAESRLDILINN 160
      VY+ACRD + E      +I      + NQ+ R LDL +S+R F + F AEE L +LINN
Sbjct: 68 VYLACRDVEKGELVAKEIQTTTGNQQVLVRKLDLSDTKSIRAFAGFLAEKHLHVLINN 127
```

```
Query: 161 AGVMACPRRTLADGFEQQFGVNHGLHFLLTNLLDRLKHSSPSRIVVSSAAHLFGRINR 220
      AGVM CP + TADGPE GVNHLGHFLLT+LLL++LK S+PSRIV VSS AH GRI+
Sbjct: 128 AGVMMCPYSKTADGFEMHIGVNHGLHFLTLHLLLEKLKESAPSRIVNVSSLAHHLGRIHF 187
```

```
Query: 221 EDLMSEKNYSKFFGAYSQSKLANILFTLKLSTILKDTGVTVNCCHPGVV RTEINRHFSGP 280
      +L EK Y+      AY SKLANILFT +L+ LK +GVT      HPG V++E+ RH S
Sbjct: 188 HNLQGEKFYNAGL-AYCHSKLANILFTQELARRLKGSGVTTYSVHPGTVQSELVRHSSFM 246
```

```
Query: 281 GWMKTALQKGSLYFFKTPKAGAQTQLRLALDPQLEGSTGGYSDCMRWPLFPWVRNMQTA 340
      WM          +F KTP+ GAQT L AL LE +G ++SDC      + RN A
Sbjct: 247 RWMWWLFS----FFIKTPQQAQTSLHCALTEGLEILSGNHFS DCHVAWVSAQARNETIA 302
```

```
Query: 341 DWLWRESEKLLGLP 354
      LW S LLGLP
Sbjct: 303 RRLWDVSCDLLGLP 316
```

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FIGURE 4. CLUSTAL X (1.81) multiple sequence alignment

```
CGI-82      PGKVVVVTGANTGIGKETAKELAQRGARVYLACRDVEKGELVAKEIQTTTGNQ-----
XP_085058   PGKVVVITGANTGIGKETARELASRGARVYIACRDVLKGESAASEIRVDTKNS-----
cg3842      DGKVVIVTGCNTGIGKETVLELAKRGARVYMACRDPGRCEAARLDIMDRSRNQ-----
PAN2        HGKTVLITGANSGLGRATAAELLRLGARVIMGCRDRARAEEAAGQLRRELQAAECGPEP
           *:. :.*.* **:. *. *:  *. * :.*.* : * . :. :

CGI-82      -----QVLVRKLDLSDTKSIRAFAGFLAEK-HLHVLINNAGVMMCPYS-KTADGFEM
XP_085058   -----QVLVRKLDLSDTKSIRAFAGFLAEK-QLHILINNAGVMMCPYS-KTADGFET
cg3842      -----QLFNRTLDLGSLSQSVRNFRVERFKAES-RLDILINNAGVMACPRT-LTADGFEQ
PAN2        GVSGVGELIVRELDLASLRVRAFCQEMLOEEP-RLDVLINNAGIFQCPYM-KTEDGFEM
           ::: * *** . *: * : *: :*:*****:: ** * **:*

CGI-82      HIGVNH LGHFLLTHLLLEKLKESAPSRIVNVSSLAHHLGRIHFHNLQGEKFYNAGL-AYC
XP_085058   HLGVNH LGHFLLTYLLLERLKVSAPARVVNVSSVAHHIGKIPFHDLOSEKRYSRGF-AYC
cg3842      QFGVNH LGHFLLTNLLLDRLKHSSPSRIVVSSAAHLFGRINREDLMSEKNYSKFFGAYS
PAN2        QFGVNH LGHFLLTNLLLGLLKSSAPSRIVVSSKLYKYGDINFDDLNSEQSYNKSF-CYS
           :*:****:***** *** ** :*:*: * ** : * * :* .*: * . :.*.

CGI-82      HSKLANILFTQELARRLKSGSVTTYSVHPGTVQSELVRHSS----FMRMWWLFS----
XP_085058   HSKLANVLFTRRELAKRLQGTGVTTYAVHPGVVRSELVRHSS----LLCLLWLRF----
cg3842      QSKLANILFTLKLSTILKDTGVTVNCCHPGVVRTEINRHFS----GPGWMKTALQ-K-GS
PAN2        RSKLANILFTRELARRLEGTVNVTNVLHPGIVRTNLGRHIH----IPLLVKPLFN--LVS
           :*****:*** :*: *. :*.*** ** * * :*: * :

CGI-82      -FFIKTPQQAQTSLHCALEGLEILSGNHFS DCHVA
XP_085058   -PFVKTAREGAQTSLHCALEGLEPLSGKYFSDCKRT
cg3842      LYFFKTPKAGAQTQLRLALDPQLEGSTGGYSDCMRW
PAN2        WAFFKTPVEGAQTSIYLASSPEVEGVSGRYFGDCKEE
           :.*.*. ***** : * : : * :*.***
```

Figure 5. Sequences of the human proteins of the invention**Figure 5A. Nucleic acid sequence of human unnamed protein XP_085058 (SEQ ID NO:1)**

```
1  aggactgtat gctgttctta aggactctct gcttcctgga caagctcaag ctaaggacta
61  catctcccag caggctgtgc tctgacagct cttggattta aataggattc tgggctctgc
121 tcagagtcag gctgctgctc agcaccagc acggagagga gcagagaagc agcagaagca
181 gccaaagagc ggagccagac caggaacctg agccagagct ggggttgaag ctggagcagc
241 agcaaaagca acagcagcta cagaagtgg aacgatgctg gtcaccttgg gactgctcac
301 ctcttctctt tcgttcctgt atatggtagc tccatccatc aggaagttct ttgctggtgg
361 agtgtgtaga acaaatgtgc agcttcctgg caaggtagtg gtgatcactg gcgccaacac
421 gggcattggc aaggagacgg ccagagagct cgctagccga ggagcccgag tctatatatgc
481 ctgcagagat gtactgaagg gggagtctgc tgccagtga atccgagtgg atacaaagaa
541 ctcccagggt ctggtgcgga aattggacct atccgacacc aaatctatcc gagcctttgc
601 tgagggtctt ctggcagagg aaaagcagct ccatattctg atcaacaatg cgggagtaat
661 gatgtgtcca tattccaaga cagctgatgg ctttgaaacc cacctgggag tcaaccacct
721 gggccacttc ctctcacct acctgctcct ggagcggcta aagggtgtctg cccctgcacg
781 ggtggttaat gtgtcctcgg tggctcacca cattggcaag attcccttcc acgacctcca
841 gagcgagaag cgctacagca ggggttttgc ctattgccac agcaagctgg ccaatgtgct
901 ttttactcgt gagctggcca agaggctcca aggcaccggg gtcaccacct acgcagtgc
961 cccaggcgct gtccgctctg agctggtccg gcactcctcc ctgctctgcc tgcctggtgc
1021 gctcttctcc ccctttgtca agacggcacg ggagggggcg cagaccagcc tgcactgcgc
1081 cctggctgag ggctggagc ccctgagtgg caagtacttc agtgactgca agaggacctg
1141 ggtgtctcca agggcccgaa ataacaaaac agctgagcgc ctatggaatg tcagctgtga
1201 gcttctagga atccggtggg agtagctggt ggaagagctg cagctttatc aggcccaatc
1261 catgccataa tgaacaggga ccaaggagaa ggccaaccct aaaggattgt cctcttggcc
1321 agctggtgct gcgaatcctg cctgctctga tcctcttgac ccttctggga atgtttgcac
1381 acctgacact cttgtgagac tggcttatgg catgagttgt ggacacctat agagtgttct
1441 tctctaagac ctggaaagtc agcaaccctc tgggggcagc aggactgggc agatcccagg
1501 ctgggcatgg ggggtggcaga agagcccgag aaattgggtc agttccctca tcagcaccag
1561 aggctcagct gaggcaagaa gagcaccatc actgcctatt tctaggggct atacactcca
1621 actcttggtt gatctctttc tttttaaaaa tttttgccac caccctggag tctagaccaa
1681 cacacaaaga tcctggctaa ccctggccta ttttagattcc ttctctcac ctggaccttc
1741 ccatttcaat catgcagatg gtttcttttt gtaaagagtt ccgtttgcct ttcaattttt
1801 agagaaaata aagactgcat tcactc
```

Figure 5B. Amino acid sequence of human unnamed protein XP_085058 (SEQ ID NO:2)

```
1  mlvtlglits ffsflymvap sirkffaggv crtnvqlpgk vvvitgantg igketarela
61  srgarvyiac rdvlkgesaa seirvdtkns qvlvrkldls dtksirafae gflaekqlh
121 ilinnagvmm cpysktadgf ethlgvnhlg hfllytllle rlvksaparv vnvssvahhi
181 gkipfhdlqs ekrysrgfay chsklanvlf trelakrlqg tgvttiyavhp gvvrselvrh
241 sslclllwrl fspfvktare gaqtslhcal aegleplsgk yfsdckrtwv sprarnnkta
301 erlwnvscel lgirwe
```

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Figure 5C. Nucleic acid sequence of human protein CGI-82 (SEQ ID NO:3)

```

1  gctggagcat cccgctctgg tgccgctgca gccggcagag atggttgagc tcatgttccc
61  gctgttgctc ctcttctgct ccttccttct gtatatggct gcgccccaaa tcaggaaaat
121 gctgtccagt ggggtgtgta catcaactgt tcagcttcct gggaaagtag ttgtggtcac
181 aggagctaatacaggtatcg ggaaggagac agccaaagag ctgggtcaga gaggagctcg
241 agtatattta gcttgccggg atgtggaaaa gggggaattg gtggccaaag agatccagac
301 caccgacagg aaccagcagg tgttggtgct gaaactggac ctgtctgata ctaagtctat
361 tcgagctttt gctaagggct tcttagctga ggaaaagcac ctccacgttt tgatcaacaa
421 tgcaggagtg atgatgtgtc cgtactcgaa gacagcagat ggctttgaga tgcacatagg
481 agtcaaccac ttgggtcact tctcctaacc ccatctgctg ctagagaaac taaaggaatc
541 agccccatca aggatagtaa atgtgtcttc cctcgacacat cacctgggaa ggatccactt
601 ccataaacctg cagggcgaga aattctacaa tgcaggcctg gcctactgtc acagcaagct
661 agccaacatc ctcttcaccc aggaactggc ccggagacta aaagggtctg gcgttacgac
721 gtattctgta caccctggca cagtccaatc tgaactggtt cggcactcat ctttcatgag
781 atggatgtgg tggcttttct ctttttctat caagactcct cagcaggagg cccagaccag
841 cctgcactgt gccttaacag aaggctctga gattctaagt gggaatcatt tcagtgaactg
901 tcatgtggca tgggtgtctg tccaagctcg taatgagact atagcaaggc ggctgtggga
961 cgtcagttgt gacctgctgg gcctcccaat agactaacag gcagtgccag ttggacccaa
1021 gagaagactg cagcagacta cacagtactt cttgtcaaaa tgattctcct tcaaggtttt
1081 caaaaccttt agcacaaaaga gagcaaaacc ttccagcctt gcctgcttgg tgtccagtta
1141 aaactcagtg tactgccaga ttctgtctaaa tgtctgtcat gtccagattt actttgcttc
1201 tgttactgcc agagttacta gagatatcat aataggataa gaagaccctc atatgacctg
1261 cacagctcat tttccttctg aaagaaacta ctacctagga gaatctaagc tatagcaggg
1321 atgatttatg caaatttgaa ctagcttctt ttttcacaat tcagttcctc ccaaccaacc
1381 agtcttctact tcaagagggc cacactgcaa cctcagctta acatgaataa caaagactgg
1441 ctcaggagca gggcttgccc aggcattggtg gatcaccgga ggtcagtagt tcaagaccag
1501 cctggccaac atgggtgaaac ccacactcta ctaaaaattg tgtatatctt tgtgtgtctt
1561 cctgtttatg tgtgccaagg gagtattttc acaaagttca aaacagccac aataatcaga
1621 gatggagcaa accagtgcc tccagtcttt atgcaaatga aatgctgcaa agggaagcag
1681 attctgtata tgttggtaac taccaccaa gagcacatgg gtagcaggga agaagtaaaa
1741 aaagagaagg agaatactgg aagataatgc acaaaatgaa gggactagtt aaggattaac
1801 tagcccttta aggattaact agttaaggat taatagcaaa agatattaaa tatgctaaca
1861 tagctatgga ggaattgagg gcaagcacc caggactgat aggtcttaac aaaaaccagt
1921 gtggcaaaaa aaaaaaaaaa aaaaaaaaaa aaaaatccta aaaacaaaca acaaaaaaaa
1981 acaattcttc attcagaaaa attatcttag ggactgatat tggtaattat ggtcaattta
2041 ataataatattt ggggcatttc cttacattgt cttgacaaga ttaaaatgtc tgtgcaaaaa
2101 ttttgtattt tatttgagga cttcttatca aaagtaatgc tgccaaagga agtctaagga
2161 attagtagtg ttcccatcac ttgtttggag tgtgctattc taaaagattt tgatttcctg
2221 gaatgacaat tataatttaa ctttgggtgg ggaagagtt ataggaccac agtcttctact
2281 tctgatactt gttaaattaat cttttattgc acctgttttg accattaagc tatatgttta
2341 gaaatgggtca ttttacggaa aaattagaaa aattctgata atagtgcaga ataaatgaat
2401 taatgtttta cttaatttat attgaactgt caatgacaaa taaaattct ttttgattat
2461 tttttgtttt catttaccag aataaaaact aagaattaaa agtttgatta cagtcaaaaa
2521 aaaaaaaaaa aaaaaaaa

```

Figure 5D. Amino acid sequence of human protein CGI-82 (SEQ ID NO:4)

```

1  mvelmfplll lllpfllyma apqirkmlss gvctstvtqlp gkvvvvtgan tgigketake
61  laqrgarvyl acrdvekgel vakeiqtttg nqqlvrkld lsdtksiraf akglflaeekh

```

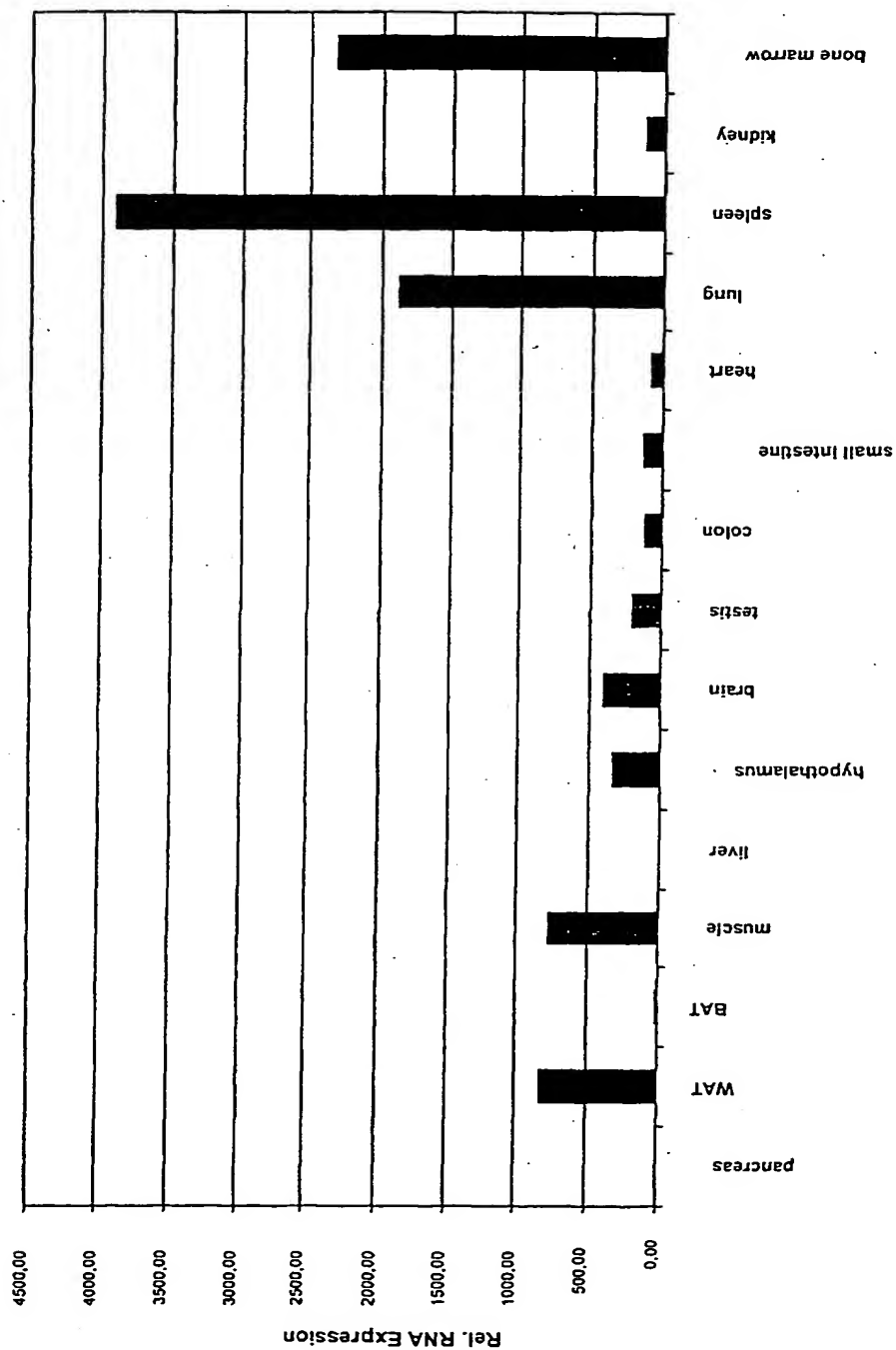
8/22

121 lhvlinnagv mmcpysktad gfemhigvnh lghfllthll leklkesaps rivnvsslah
181 hlgrihfhn1 qgekfyngl aychsklani lftqelarri kgsgvttysv hpgtvqsely
241 rhssfmrmw wlfsffiktp qggaqtslhc altegileils gnhfsdchva wsvqarnet
301 iarrlwvsc dllglpid

9/22

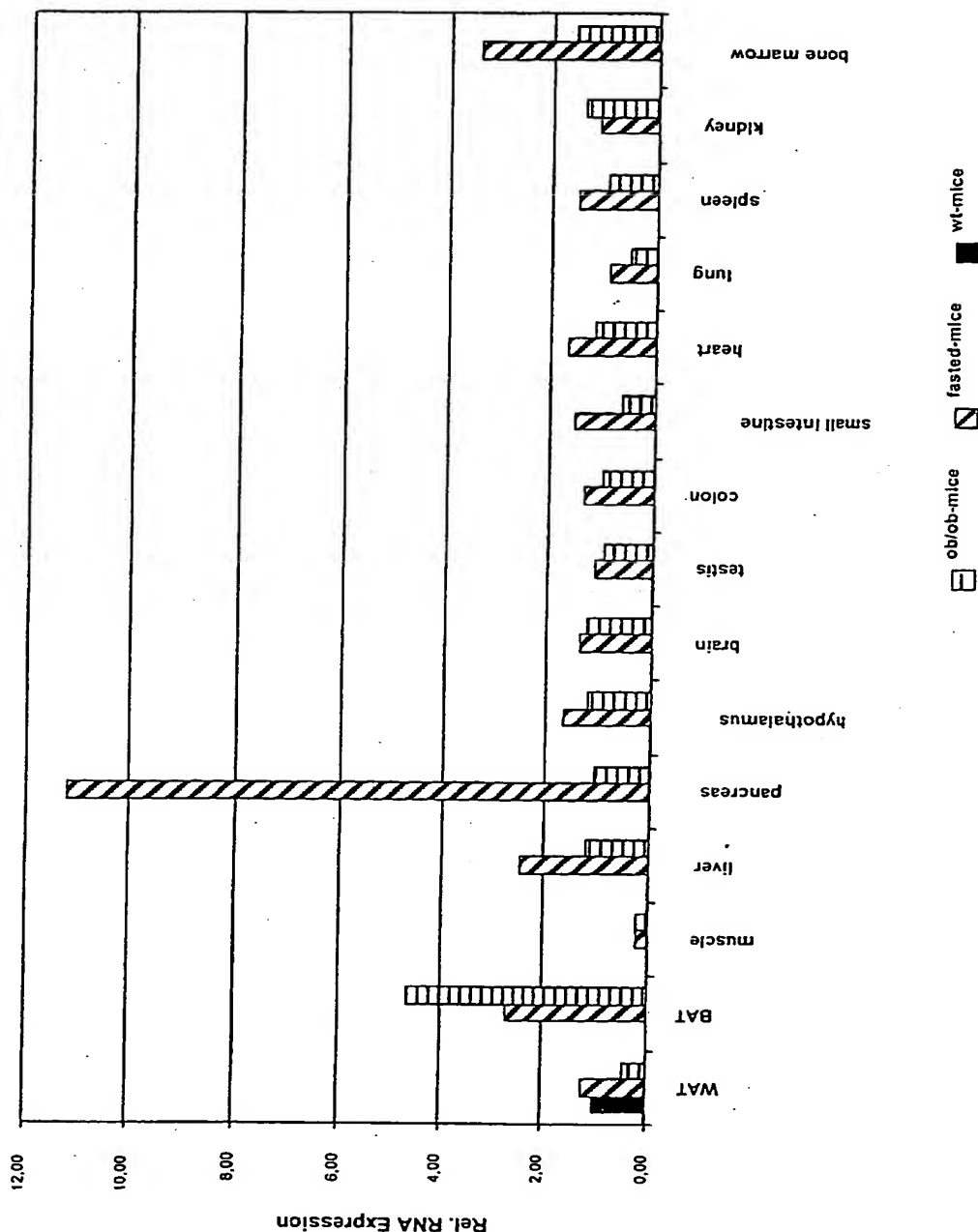
FIGURE 6. Expression of unnamed protein (DG21-1) in mammalian tissues

FIGURE 6A. Real-time PCR analysis of unnamed protein (DG21-1) in wildtype mouse tissues.



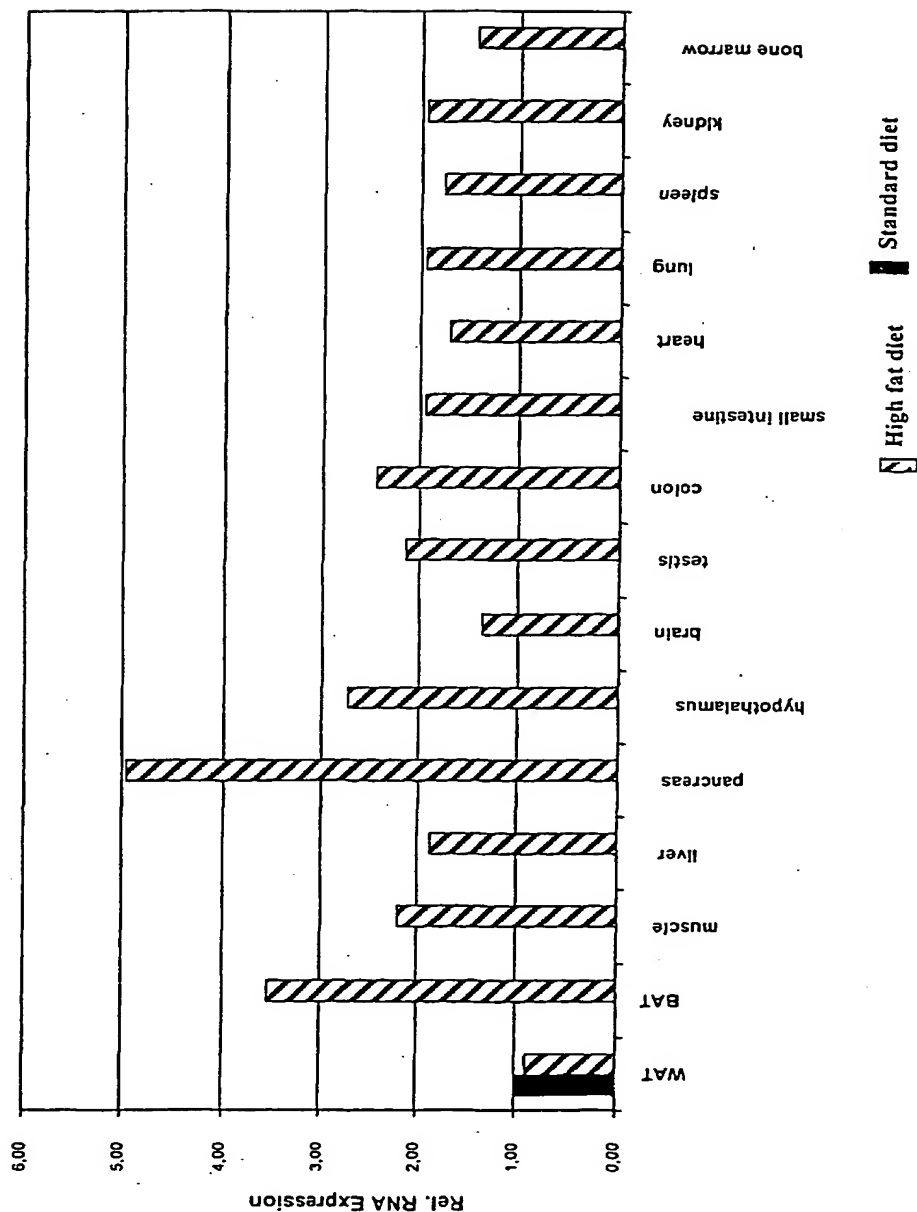
10/22

FIGURE 6B. Real-time PCR mediated analysis of unnamed protein (DG21-1) in different mouse models.



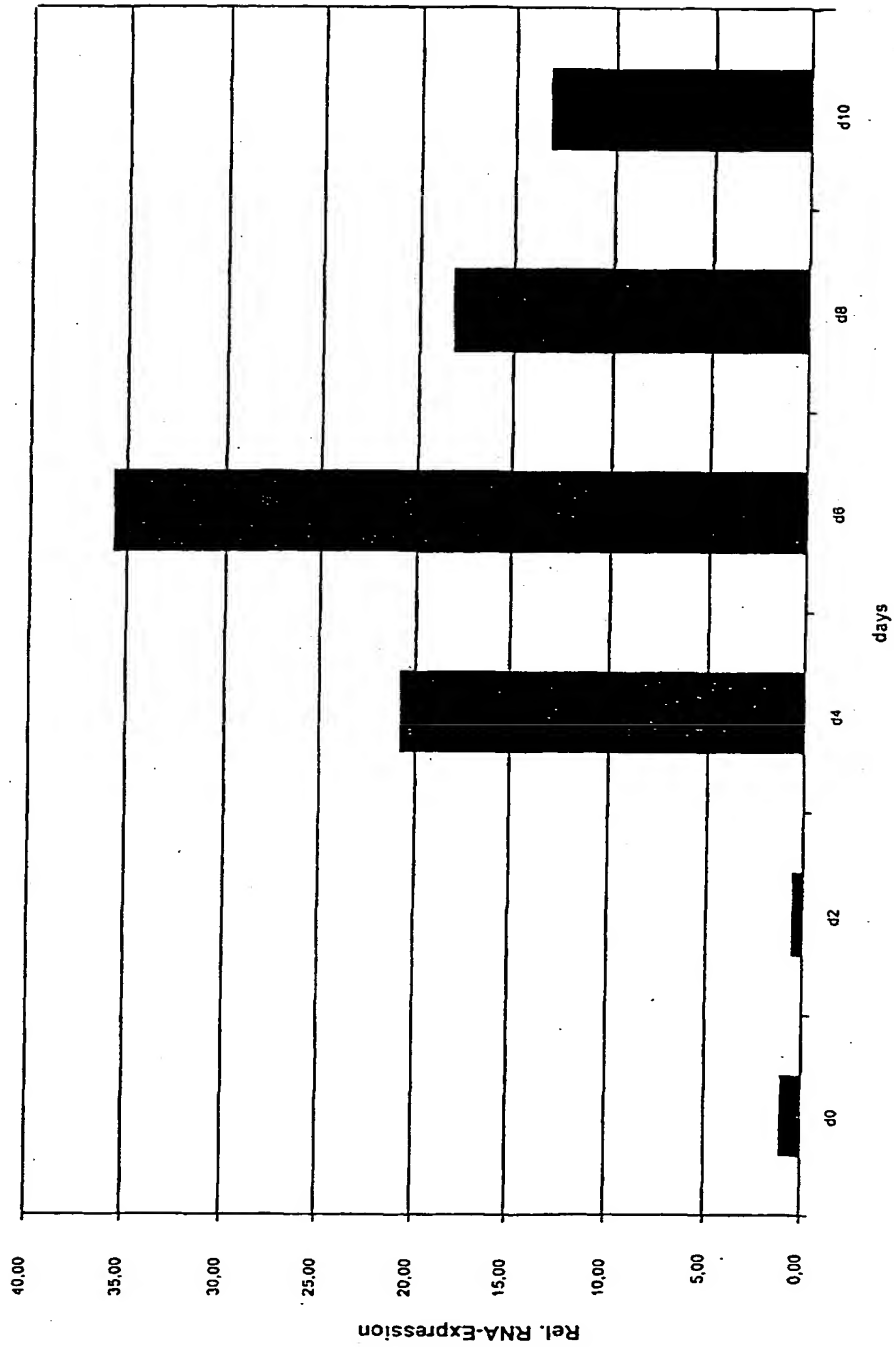
11/22

FIGURE 6C. Real-time PCR mediated analysis of unnamed protein (DG21-1) in different mouse models (different diets).



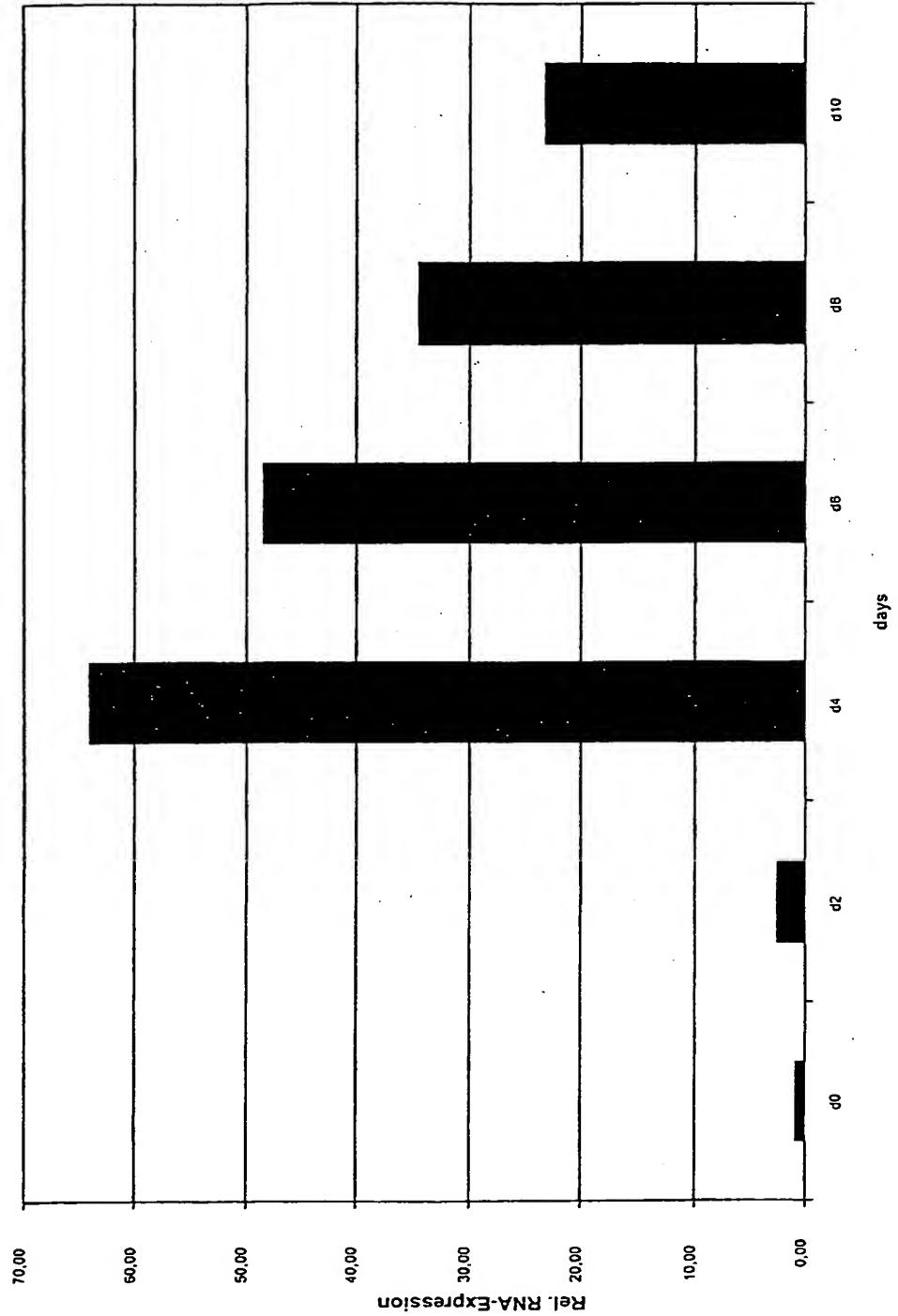
12/22

FIGURE 6D. Real-time PCR mediated analysis of unnamed protein (DG21-1) expression during the differentiation of 3T3-L1 cells from preadipocytes to mature adipocytes.



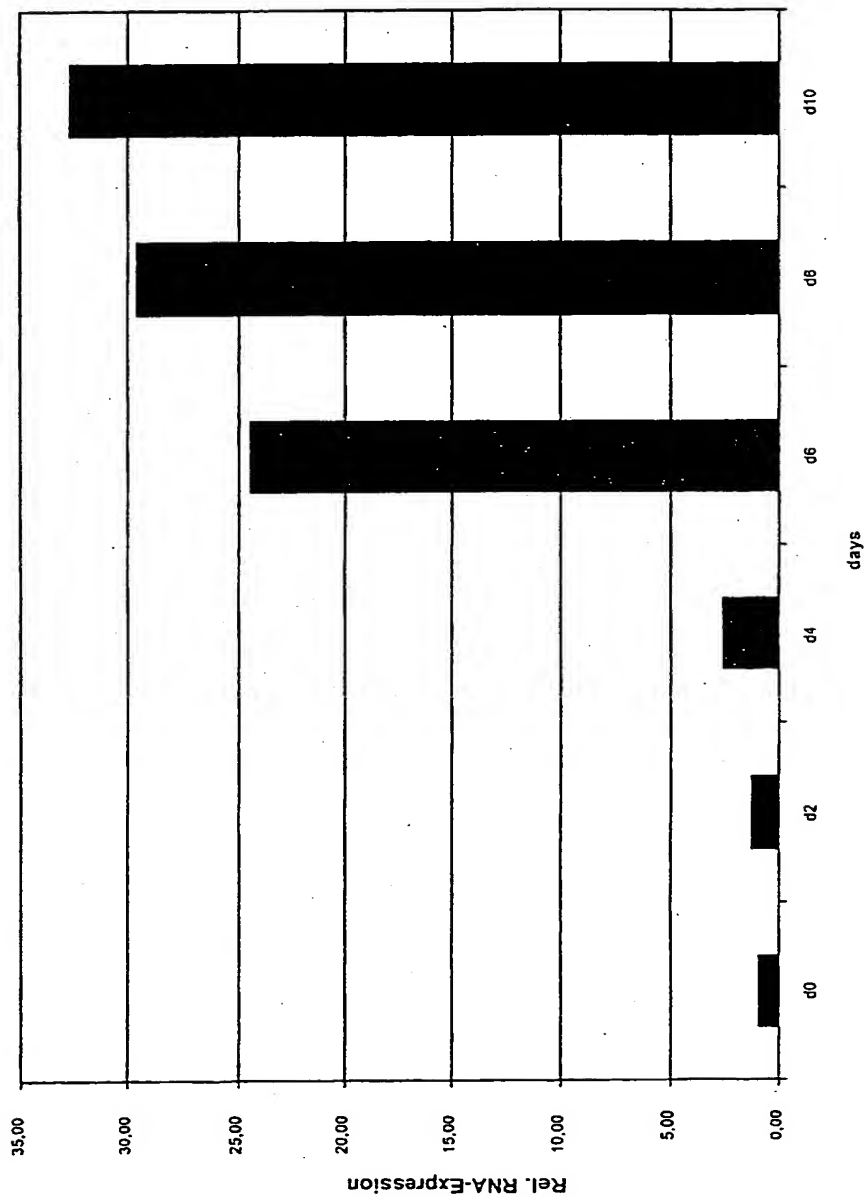
13/22

FIGURE 6E. Real-time PCR mediated analysis of unnamed protein (DG21-1) expression during the differentiation of 3T3-F442A cells from preadipocytes to mature adipocytes.



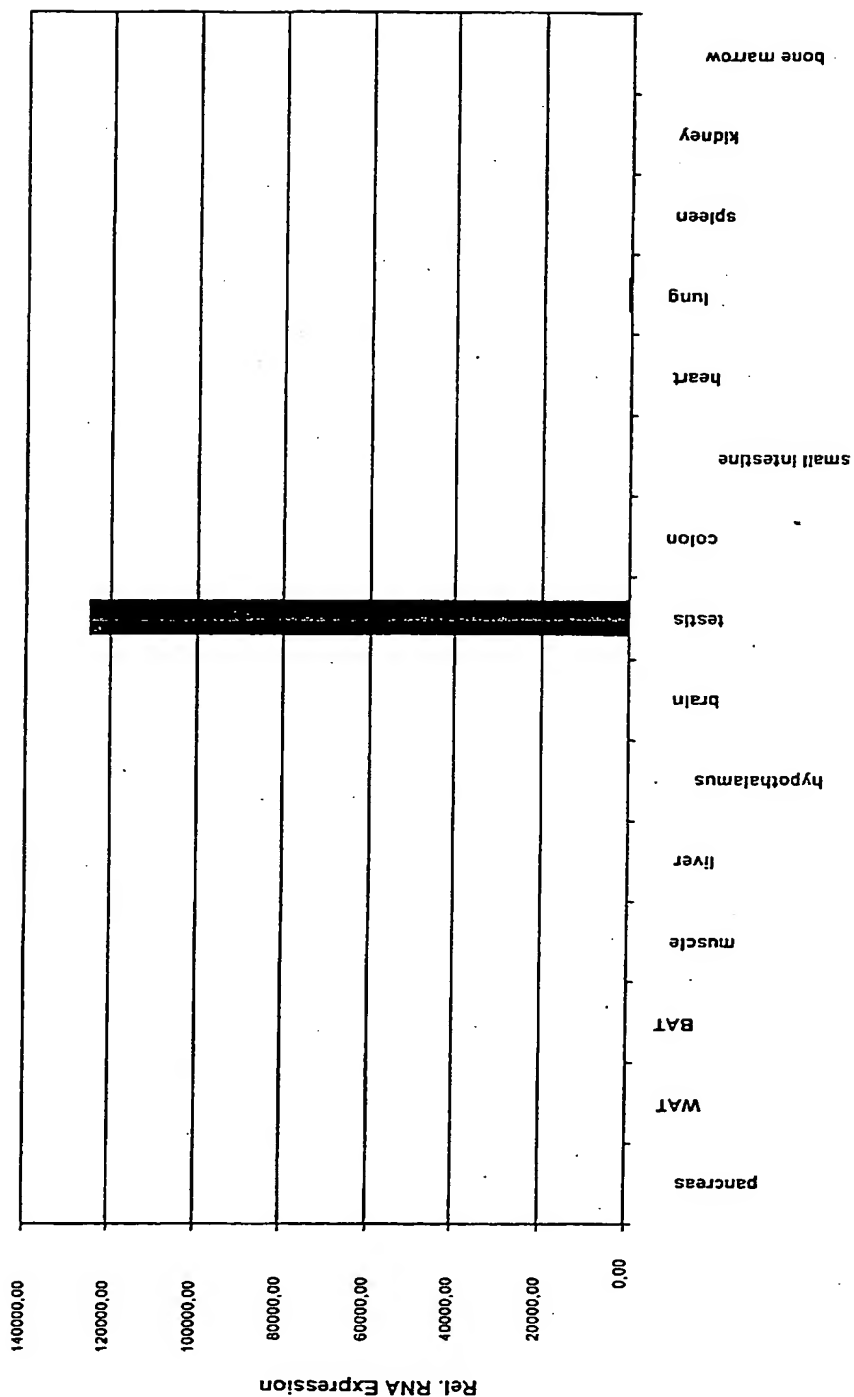
14/22

FIGURE 6F. Real-time PCR mediated analysis of unnamed protein (DG21-1) expression during the differentiation of TAI cells from preadipocytes to mature adipocytes.



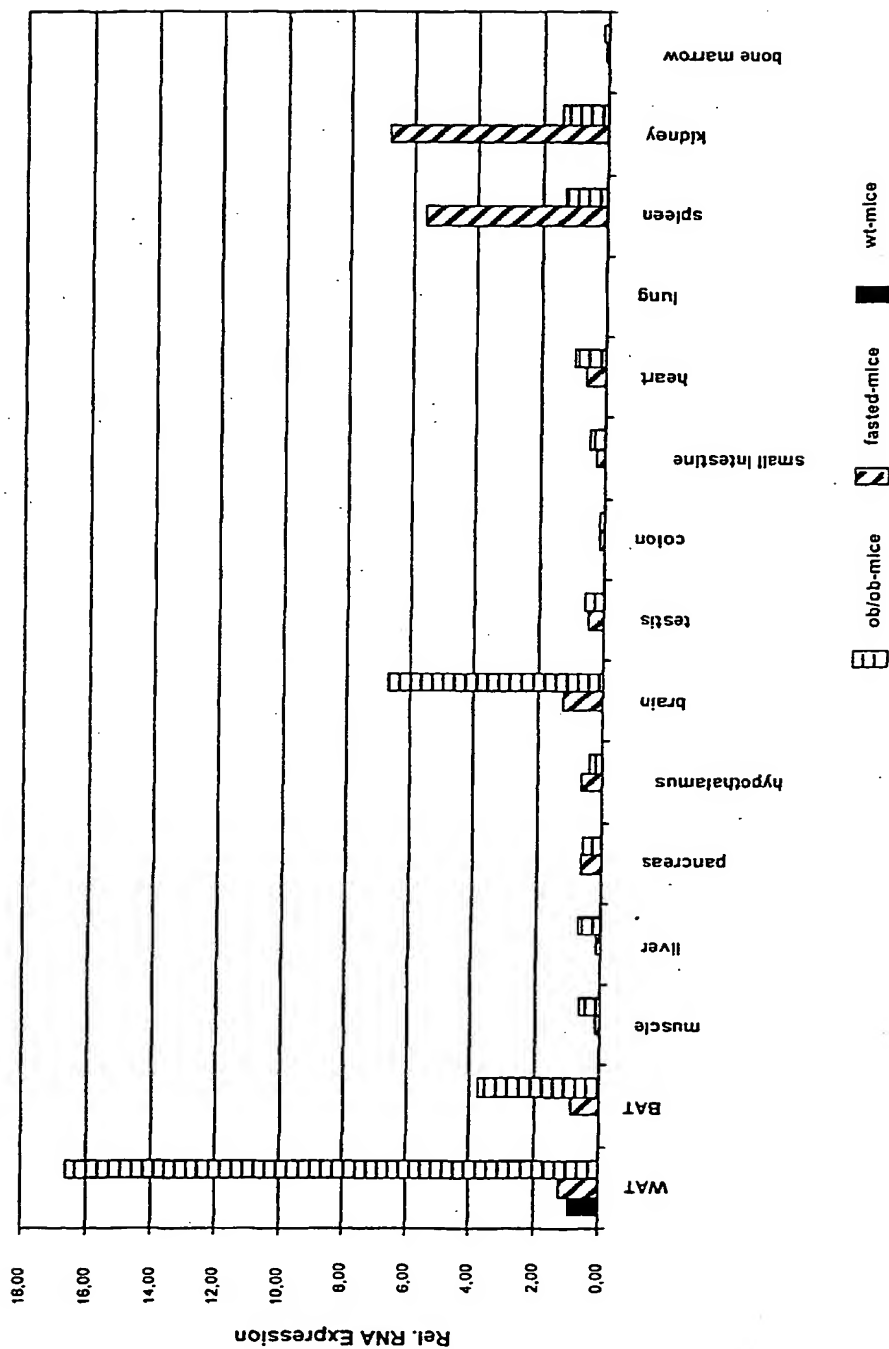
15/22

FIGURE 7. Expression of CGI-82 (DG21-2) in mammalian tissues
FIGURE 7A. Real-time PCR analysis of CGI-82 (DG21-2) in wildtype mouse tissues.



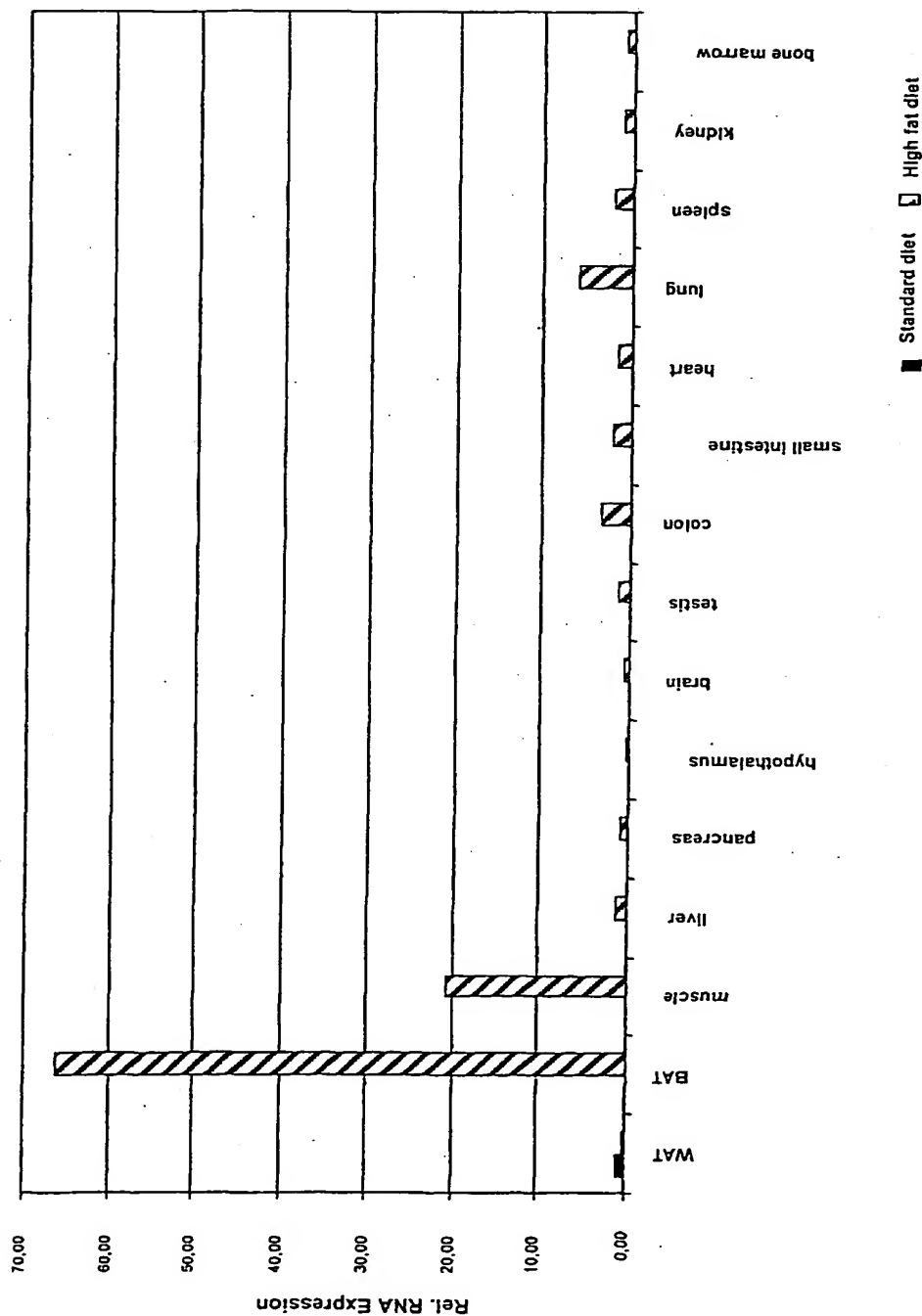
16/22

FIGURE 7B. Real-time PCR mediated analysis of CGI-82 (DG21-2) in different mouse models.



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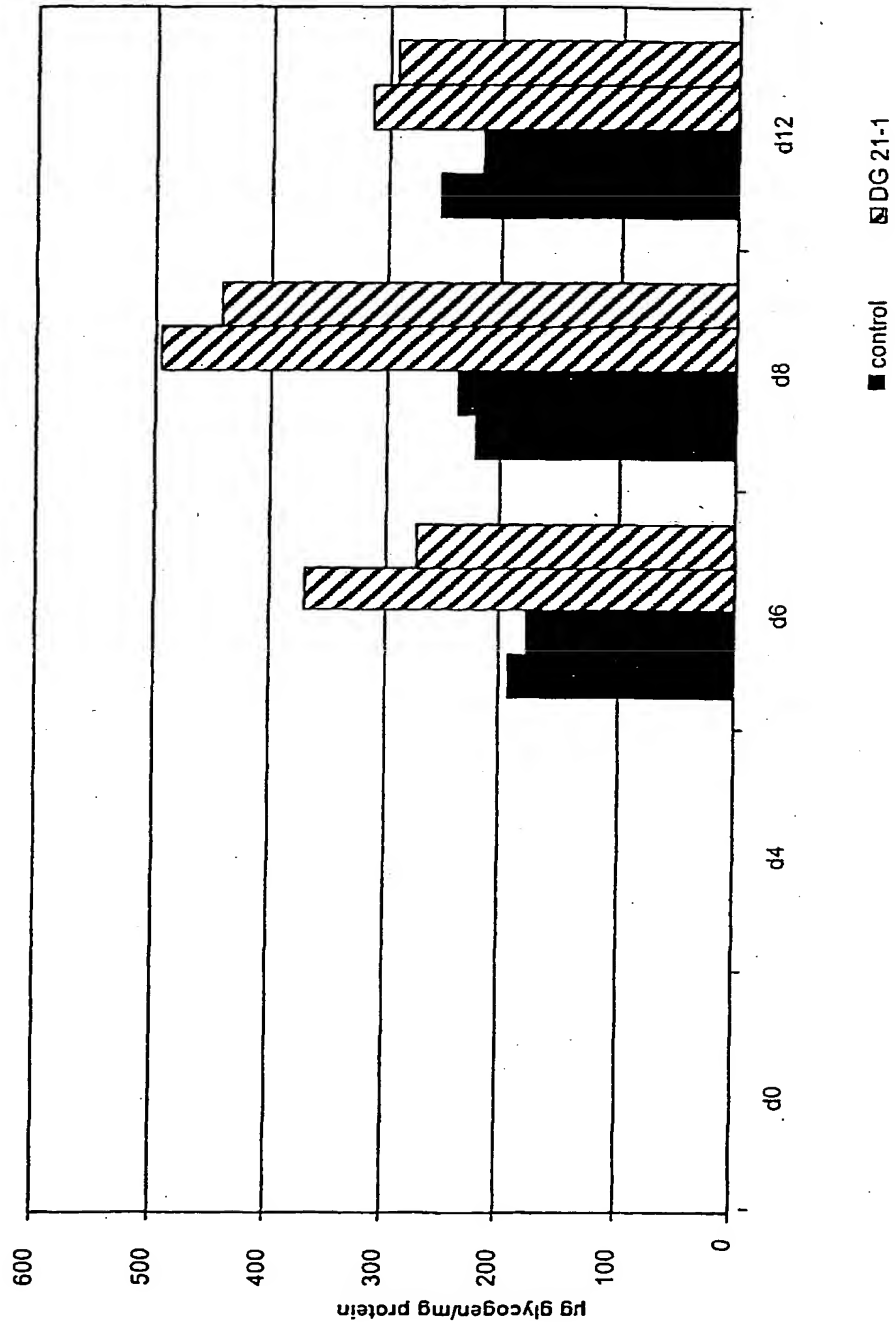
FIGURE 7C. Real-time PCR mediated analysis of CGI-82 (DG21-2) in different mouse models
(different diets)



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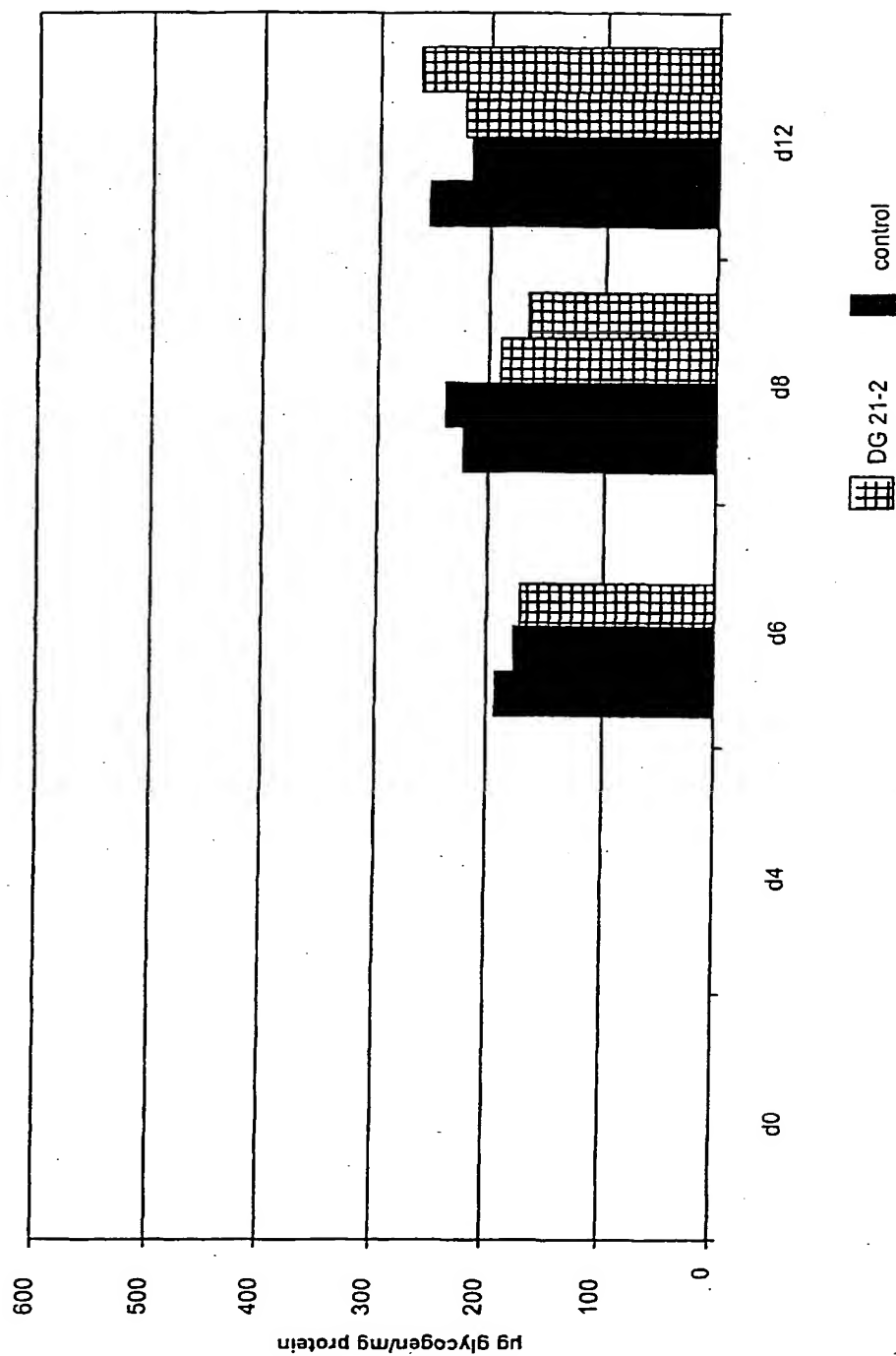
FIGURE 8. In vitro assays for the determination of Energy Storage Metabolites in cells overexpressing unnamed protein (DG21-1) or CGI-82 (DG21-2)

FIGURE 8A. Glycogen levels in cells overexpressing unnamed protein (DG21-1)



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FIGURE 8B. Glycogen levels in cells overexpressing CGI-82 (DG21-2)



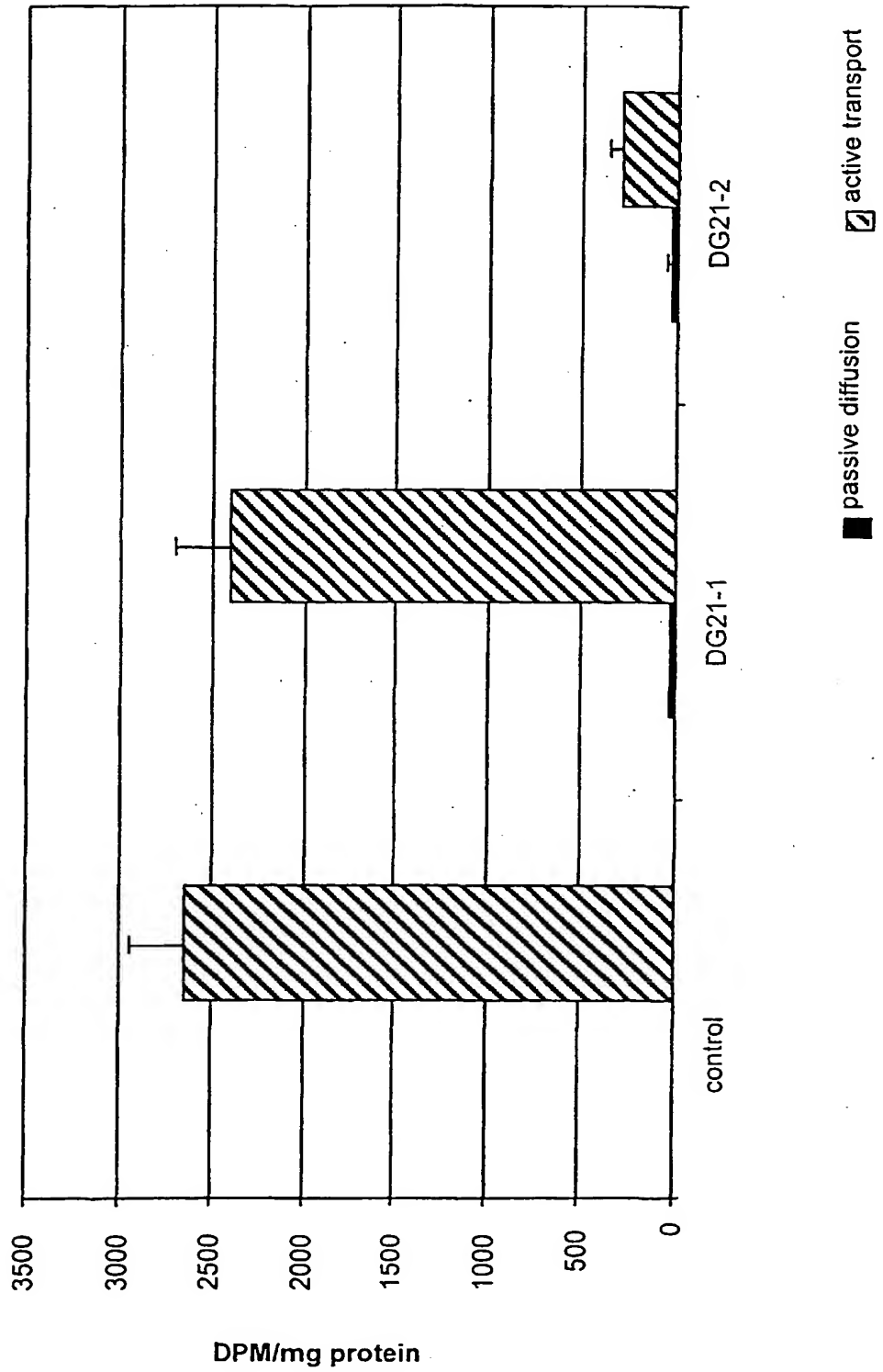
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FIGURE 8C. Free fatty acid uptake in cells overexpressing unnamed protein (DG21-1) or CGI-82 (DG21-2)



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FIGURE 8D. Esterified free fatty acids in cells overexpressing unnamed protein (DG21-1) or CGI-82 (DG21-2)



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FIGURE 8E. Lipid synthesis in cells overexpressing unnamed protein (DG21-1) or CGI-82 (DG21-2) with or without insulin stimulation

